

PATENT
USSN 08/974,584
015389-002950US
018/206p2

APPENDIX A

BEST AVAILABLE COPY

Mouse TERT protein sequence

LOCUS 070372 1122 aa linear ROD 15-JUN-2002
DEFINITION Telomerase reverse transcriptase (Telomerase catalytic subunit).
ORGANISM Mus musculus
AUTHORS Greenberg,R.A., Allsopp,R.C., Chin,L., Morin,G.B. and DePinho,R.A.
TITLE Expression of mouse telomerase reverse transcriptase during development, differentiation and proliferation
JOURNAL Oncogene 16 (13), 1723-1730 (1998)

1 mtraprcpav rsl1rsryre vwplatfvrr lgpegrrlvq pgdpkiyrtl vaqclvcmh
61 gsqqppadls fhqvssikel varvvqrilce rnernvalgf fellneargg ppmafstssvr
121 sylpnvtviet lrvsgawmll lsrvgddllv yllahcally lvppscayqv cgsplqica
181 ttdiwpvsas syrprpvgr nftnlrlflqq iksssrqeap kplalpsrgt krh1s1tsts
241 vpsakkarcy pvprveegph rqvlptpsgk swvpsparsp evptaekdls skgkvds1s1
301 sgsvcckhkp ssst11sppr qnafqlrpfi ethrflysrq dgqerlnpsf 11sn1qpnl1
361 garrlveiif lgsrprtsgp lcrthrlsrr ywqmrplfqq 11vnhaecqy vr11rshcrf
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481 1kkfislgky gk1s1qelmw kmkvedchwl rsspgkd1rvp aae1rlrer1 latflfw1md
541 tyvvq11rsf fyitestf1qk nr1ffyrk1sv wsk1lqs1g1v qh1erv1r1re 1s1qeevrhhq
601 dtwlampicr 1rf1pkp1ng1 rpi1vnmsysm g1ralgrkq aqhf1qr1kt 1fsmlnyert
661 khph1mgssv lgmnd1yrtw raf11rvral dqtprmyfvk advtg1aydai pqgk11vevva
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 018/206p2

SEQ. ID NO:124 (Figure 60)

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ORF Finder (Open Reading Frame Finder)

PubMed

Entrez

BLAST

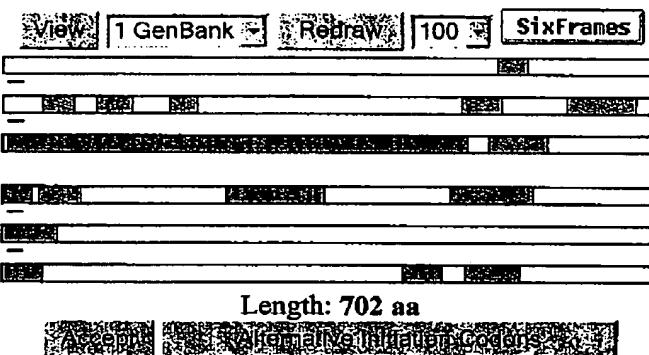
OMIM

Taxonomy

Structure

Anonymous

Program **blastp** Database **nr** BLAST with parameters **Cognitor**



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78 agccgataccgggagggtgtggccgcgtggcaaccttgcggcgc
 S R Y R E V W P L A T F V R R
123 ctggggcccgagggcaggccgttgcacaacccggggaccgcag
 L G P E G R R L V Q P G D P K
168 atctaccgcacttgggtgcccattgcctagtgtgcattgcactgg
 I Y R T L V A Q C L V C M H W
213 ggctcacagccacatggccatgcgcaccccttcaccagggtgtca
 G S Q P P P A D L S F H Q V S
258 tccctgaaagagactggccgcagggtgtgcagagactctgcgag
 S L K E L V A R V V Q R L C E
303 cgcaacgagaaaacgtgtggctttggcttgagctgcattaac
 R N E R N V L A F G F E L L N
348 gaggccagaggccgcctccatggccctcaactagtagcgtgcgt
 E A R G G P P M A F T S S V R
393 agctacttgcacaacactgttattgagaccctgcgtcagtgg
 S Y L P N T V I E T L R V S G
438 gcatggatgtactgttgcggcgtggccgcacgcacgtgtgtc
 A W M L L S R V G D D L L V
483 tacctgtggcacaactgtgtctttatcttgcgtggcccccac
 Y L L A H C A I Y L L V P P S
528 tgtgcctaccagggtgtgggtctccctgtaccaaattgtgcc
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618 cgaccctggccaggaaattcaacttaggttacaacag
 R P V G R N F T N L R F L Q Q
663 atcaagagcagttagtcgcaggaaacccctggcccttg
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Frame	from	to	Length
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-1	1040..1486		447
-1	2060..2443		384
+2	2600..2917		318
+3	2241..2510		270
-3	2127..2387		261
-2	1.. 258		258
-1	170.. 370		201
-3	1.. 191		191
+2	2117..2302		186
-3	1842..2018		177
+2	440.. 604		165
+2	191.. 337		147
-1	2.. 139		138
+1	2281..2415		135
+2	776.. 907		132

708 ccatctcgaggatcaaagaggcatctgagtctcaccagtacaagt
P S R G T K R H L S L T S T S
753 gtgccttcagtaagaaggccagatgttatctgtcccggagatg
V P S A K K A R C Y P V P R V
798 gagggaggaccccacaggcagggtgctaccaacccatcaggcaaa
E E G P H R Q V L P T P S G K
843 tcatgggtgccaagtcctgtcggtccccggagggtgcctactgca
S W V P S P A R S P E V P T A
888 gaaaaagatttgtttctaaaggaaagggtgtctgacctgagtc
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933 tctgggtcggtgtctgtaaaacacaagccagctccacatctcg
S G S V C C K H K P S S T S L
978 ctgtcaccaccccgccaaaatgccttcagctcaggccatttatt
L S P P R Q N A F Q L R P F I
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1068 ctaaacccctcattcctactcagcaacctccagcctaacttgact
L N P S F L L S N L Q P N L T
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S L W G T R H N E R R F F K N
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D X T P X C T L L R Q M



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION TBLASTN 2.2.13 [Nov-27-2005]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**

x_dropoff: **50** expect: **10.000** wordsize: **3** Filter View option **Standard**

Masking character option **X** for protein, **n** for nucleotide Masking color option **Black**

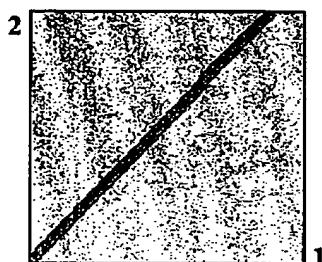
Show CDS translation

Sequence 1: lcl|seq_1

Length = 1122 (1 .. 1122)

Sequence 2: lcl|seq_2

Length = 3025 (1 .. 3025)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

[REDACTED]

Score = 1595 bits (4129), Expect = 0.0
 Identities = 830/1001 (82%), Positives = 840/1001 (83%), Gaps = 22/1001 (2%)
 Frame = +3

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Sbjct 33	MTRAPRPCAVRSLLRSRYREVWPLATFVRRRLGPEGRRRVQPGDPKIFYRTLVAQCLVCMHW	212
Query 61	GSQPPP PADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	120
Sbjct 213	GSQPPP PADLSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	392
Query 121	SYLPNTVIETLRVSGAWMLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA	180
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Query 181	TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS	240
	TTDIWPSVSASYRPTRPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS	

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Sbjct	753	VPSAKKARCYCVPVPRVEEGPHRQLPTPSGKSWVPSPARSPEVPTAEKDLSKGKVSDL	932
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		GARRLVEIIIFLGSRPRTSGPLCRTTHRLSRRYWQMRPLFQQLLVNHAECQYVRLRSRCF	
Sbjct	1113	GARRLVEIIIFLGSRPRTSGPLCRTTHRLSRRYWQMRPLFQQLLVNHAECQYVRLRSRCF	1292
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Query	541	TYVVQLLRSFFYITESTFQKNRLFFYRKSVWSKLQSIGVRQHLERVRLRELSQEEVRHHQ	600
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		KHPHLMGSSVLGMNDIYRTWRAFVLRVRA LD TP ++ G P	
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Query	712	-----QGKLVEVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRQQVTTLSDLQPYMG	765
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Sbjct	2193	XXXXXXXXXXXXXXVEVVANMIRHSESTYCIRQYAVVRRDSQGQVHKSFRQQVTTFSDFQPYMG	2372
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		QFLKHLQDSDASALRNSVIEQSISSMNESSSSLF D S V + R T	
Sbjct	2373	QFLKHLQDSDASALRNSVIEQSISSMNESSSSLFDSSC---TSCVTVS*RLVTGAIRSA	2540
Query	826	QGSSLSTLL--CSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQAK-TFLSTLVH	882
		+ S + CS + ++ G+ +V L K	
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Sbjct	2721	XXCSY	2900
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CPU time: 0.10 user secs. 0.00 sys. secs 0.10 total secs.

Lambda	K	H
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PATENT
 USSN 08/974,584
 015389-002950US
 018/206p2

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mTERT:	61	GSQPPPDLFSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	120
SEQ. 124:	213	GSQPPPDLFSFHQVSSLKELVARVVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	392
mTERT:	121	SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA	180
SEQ. 124:	393	SYLPNTVIETLRVSGAWMLLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA	572
mTERT:	181	TTDIWPSVSASYRPTPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS	240
SEQ. 124:	573	TTDIWPSVSASYRPTPVGRNFTNLRFLQQIKSSSRQEAPKPLALPSRGTKRHLSLTSTS	752
mTERT:	241	VPSAKKARCYPVPRVVEEGPHRQLPTPSGKSWVPSPARSPEVPTAEKDLSKGKVSDL	300
SEQ. 124:	753	VPSAKKARCYPVPRVVEEGPHRQLPTPSGKSWVPSPARSPEVPTAEKDLSKGKVSDL	932
mTERT:	301	SGSVCKHKPSSTSLLSPRQNFAQLRFIETRHFYLSRGDGQERLNPSFLSNLQPNLT	360
SEQ. 124:	933	SGSVCKHKPSSTSLLSPRQNFAQLRFIETRHFYLSRGDGQERLNPSFLSNLQPNLT	1112
mTERT:	361	GARRLVEIIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLRSHC	420
SEQ. 124:	1113	GARRLVEIIIFLGSRPRTSGPLCRTHRLSRRYWQMRPLFQQLLVNHAECQYVRLRSHC	1292
mTERT:	421	RTANQQVTDALNTSPPHMDLLRLHSSPWQVYGLRACLCKVVSASLGTRHNERRFFKN	480
SEQ. 124:	1293	RTANQQVTDALNTSPPHMDLLRLHSSPWQVYGLRACLCKVVSASLGTRHNERRFFKN	1472
mTERT:	481	LKKFISLGKYGKLSLQELMWKMVKEDCHWLRSRSPGKDRVPAAEHLRERILATFLF	540
SEQ. 124:	1473	LKKFISLGKYGKLSLQELMWKMVKEDCHWLRSRSPGKDRVPAAEHLRERILATFLF	1652
mTERT:	541	TYVVOLLRSFFYTESTFQKNREFFYRKSVWSKLOSIGVRQHLERVRLRELSQEEVRHHQ	600
SEQ. 124:	1653	TYVVOLLRSFFYTESTFQKNREFFYRKSVWSKLOSIGVRQHLERVRLRELSQEEVRHHQ	1832
mTERT:	601	DTWLAMPICRLRFIPKPNGLRPINVMSYSMGTALGRRKQAOHFTQRLKTLFSMLNYERT	660
SEQ. 124:	1833	DTWLAMPICRLRFIPKPNGLRPINVMSYSMGTALGRRKQAOHFTQRLKTLFSMLNYEPT	2012
mTERT:	661	KHPHLMGSSVLMNDIYRTWRAFLVRLRALD	691
SEQ. 124:	2013	KHPHLMGSSVLMNDIYRTWRAFLVRLRALD	

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